EXHIBIT A

Basic Local Alignment Search Tool

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Edit and Resubmit Save Search Strategies Formatting options Download

Blast 2 sequences

dbj|BB611382.1| (591 letters)

Results for:
dbj|BB611382.1 BB611382 RIKEN full-length enriched, adult male hippocampus Mus musculus cDNA clone 2900055L15 5'.(591bp)
Your BLAST job specified more than one input sequence. This box lets you choose which input sequence to show BLAST results for.

Query ID
gi|16452632|dbj|BB611382.1|
gi|16452632|dbj|BB611382.1|
Description
BB611382 RIKEN full-length enriched, adult male hippocampus Mus musculus cDNA clone 2900055L15 5'.
Molecule type
rna
Query Length
591

Subject ID
31643
Description
None
Molecule type
nucleic acid
Subject Length
2208
Program
BLASTN 2.2.24+ Citation

Reference
Zheng Zhang, Scott Schwartz, Lukas Wagner, and Webb Miller (2000), "A greedy algorithm for aligning DNA sequences", J Comput Biol 2000; 7(1-2):203-14.
Other reports: Search Summary [Taxonomy reports]

Search Parameters

Search parameter name	Search parameter value
Program	blastn
Word size	28
Expect value	10
Hitlist size	100
Match/Mismatch scores	1,-2
Gapcosts	0,0
Low Complexity Filter	Yes
Filter string	L;m;
Genetic Code	1

Karlin-Altschul statistics

Params	Ungapped	Gapped
Lambda	1.33271	1.28
K	0.620991	0.46
H	1.12409	0.85

Results Statistics

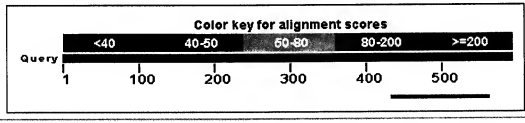
Results Statistics parameter name	Results Statistics parameter value
Effective search space	1268710

Graphic Summary

Distribution of 1 Blast Hits on the Query Sequence

[?]

An overview of the database sequences aligned to the query sequence is shown. The score of each alignment is indicated by one of five different colors, which divides the range of scores into five groups. Multiple alignments on the same database sequence are connected by a striped line. Mousing over a hit sequence causes the definition and score to be shown in the window at the top, clicking on a hit sequence takes the user to the associated alignments. New: This graphic is an overview of database sequences aligned to the query sequence. Alignments are color-coded by score, within one of five score ranges. Multiple alignments on the same database sequence are connected by a dashed line. Mousing over an alignment shows the alignment definition and score in the box at the top. Clicking an alignment displays the alignment detail.



Dot Matrix View

Plot of gi|16452632|dbj|BB611382.1| vs 31643 [?]

This dot matrix view shows regions of similarity based upon the BLAST results. The query sequence is represented on the X-axis and the numbers represent the bases/residues of the query. The subject is represented on the Y-axis and again the numbers represent the bases/residues of the subject. Alignments are shown in the plot as lines. Plus strand and protein matches are slanted from the bottom left to the upper right corner, minus strand matches are slanted from the upper left to the lower right. The number of lines shown in the plot is the same as the number of alignments found by BLAST.

Descriptions

Legend for links to other resources: U UniGene E GEO G Gene S Structure M Map Viewer PubChem BioAssay

Sequences producing significant alignments:

Accession	Description	Max score	Total score	Query coverage	E value	Max ident	Links
31643		202	202	21%	1e-55	94%	

Alignments

Select All Get selected sequences Distance tree of results Multiple alignment

```
>lcl|31643
Length=2208

 Score =  202 bits (109),  Expect = 1e-55
 Identities = 123/130 (95%), Gaps = 0/130 (0%)
 Strand=Plus/Plus

Query  432  ATGCATTGTGGGTTACTGGAGGAACCCGACATGGATTCCACAGAGAGCTGGATTGAAAGA  491
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1    ATGCATTGTGGGTTACTGGAGGAACCCGACATGGATTCCACAGAGAGCTGGATTGAAAGA  60

Query  492  TGTCTCAATGAAAGCGAGAATAAACGCTATTCCAGTCACACATCTCTGGGGAATGTGTCT  551
            |||||||| ||||| || || ||||| |||||||| |||||||||||||||||||| |||
Sbjct  61   TGTCTCAACGAAAGTGAAAACAAACGTTATTCCAGCCACACATCTCTGGGGAATGTTTCT  120

Query  552  AATGATGAAA  561
            ||||||||||
Sbjct  121  AATGATGAAA  130
```

Select All Get selected sequences Distance tree of results Multiple alignment